

ATTORNEY DOCKET NO. 07121.0003U1  
Application No. 09/990,874

**Amendments to the Specification:**

Please replace the paragraph beginning at page 9, line 6 with the following amended paragraph:

**FIGURE 1** shows an amino acid sequence alignment among Family 11 xylanases. The amino acid numbering is compared with *Trichoderma reesei* xylanase II (Tr2) as indicated at the top of the sequences. The residues at position 75 and 105 (relative to Tr2) are in italic and indicated with an asterisk. The amino acids common to at least 75% of the listed Family 11 xylanases are indicated in bold. The residues common to all Family 11 xylanases are underlined. For xylanases with a cellulose-binding domain, only the catalytic core sequences are presented. Bp: *Bacillus pumilus* (SEQ ID NO:4); Ca: *Clostridium acetobutylicum* P262 XynB (SEQ ID NO:6); Cs: *Clostridium stercorarium* xynA (SEQ ID NO:7); Rf: *Ruminococcus flavefaciens* (SEQ ID NO:8); Tr2 *Trichoderma reesei* XYN II (SEQ ID NO:16); Tv: *Trichoderma viride* (SEQ ID NO:17); Th: *Trichoderma harzianum* (SEQ ID NO:14); Sc: *Schizophyllum commune* Xylanase A (SEQ ID NO:9); An: *Aspergillus niger*, var. *awamori* (SEQ ID NO:1); Ak: *Aspergillus kawachii* XynC (SEQ ID NO:54); At: *Aspergillus tubigensis* (SEQ ID NO:2); Tr1: *Trichoderma reesei* XYN I (SEQ ID NO:15); Aa: *Aspergillus awamori* var. *kawachi* Xyn B (SEQ ID NO:19); Fs: *Fibrobacter succinogenes* XYN II (SEQ ID NO:18); Ss: *Streptomyces* sp. 36a (SEQ ID NO:12); SIB: *Streptomyces lividans* Xln B (SEQ ID NO:10); SIC: *Streptomyces lividans* Xln C (SEQ ID NO:11); TI: *Thermomyces lanuginosus* Xyn (SEQ ID NO:20); Tf: *Thermomonospora fusca* TfxA (SEQ ID NO:13); Bc: *Bacillus circulans* (SEQ ID NO:3); Bs: *Bacillus subtilis* (SEQ ID NO:5).

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*Please replace the paragraph beginning at page 16, line 24 with the following amended paragraph:*

~~These~~ The use of these two terms (thermophilicity and thermostability) has been confused within the prior art as they have been used interchangeably. However, the use of the terms as defined herein is consistent with the usage of the terms in the art (Mathrani and Ahring, 1992).

*Please replace the paragraph beginning at page 29, line 3 with the following amended paragraph:*

The construction of this precursor plasmid pTrX-HML has been described in detail in U.S. Pat. No. 5,759,840 (see Example 1N, herein incorporated by reference; plasmid termed pNI-TX13). TrX-HML comprises the native TrX xylanase, along with three mutations at N10H (Asn at position 10 is replaced with His), Y27M and N29L. The first thirty amino acids of the sequence comprising N10H, Y27M and N29L are shown below (SEQ ID NO:56, 57; DNA and amino acid, respectively).

*Please replace the paragraph on page 31, line 1 with the following amended paragraph:*

TX-105R-1 (SEQ ID NO:44 and 58; DNA and amino acid, respectively)

*Please replace the paragraph on page 31, line 8 with the following amended paragraph:*

TX-C1 (SEQ ID NO:42 and 59; DNA and amino acid, respectively)

*Please replace the paragraph on page 32, line 1 with the following amended paragraph:*

TX-75A-1 (SEQ ID NO:40 and 60; DNA and amino acid, respectively)

*Please replace the paragraph on page 32, line 7 with the following amended paragraph:*

TX-75G-1 (SEQ ID NO:46 and 61; DNA and amino acid, respectively)

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*Please replace the paragraph on page 33, line 14 with the following amended*

*paragraph:*

TX-125A129E-1 (SEQ ID NO:49 and 62; DNA and amino acid, respectively)

*Please replace the paragraph on page 34, line 12 (?) with the following amended .*

*paragraph:*

TX-105H-1 (SEQ ID NO:41 and 63; DNA and amino acid, respectively)

*Please replace the paragraph on page 35, line 13 with the following amended*

*paragraph:*

TX-del(123-144)-1r (SEQ ID NO:43 and 64; DNA and amino acid, respectively)

*Please replace the paragraph on page 35, line 19 with the following amended*

*paragraph:*

TX-N1 (SEQ ID NO:45 and 65; DNA and amino acid, respectively)

*Please replace the paragraph on page 36, line 10 with the following amended*

*paragraph:*

TX-144R-1r (SEQ ID NO:47 and 66; DNA and amino acid, respectively)

*Please replace the paragraph on page 37, line 7 with the following amended paragraph:*

TX-161R-1r (SEQ ID NO:48 and 67; DNA and amino acid, respectively)

*Please replace the paragraph on page 38, line 1 with the following amended paragraph:*

TX-116G-1 (SEQ ID NO:50 and 68; DNA and amino acid, respectively)

*Please replace the paragraph on page 38, line 7 with the following amended paragraph:*

TX-118C-1 (SEQ ID NO:51 and 69; DNA and amino acid, respectively)

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*Please replace the paragraph on page 39, line 24 with the following amended*

*paragraph:*

**TX-10H11D-1** (SEQ ID NO:52 and 70; DNA and amino acid, respectively)

*Please replace the paragraph on page 41, line 1 with the following amended paragraph:*

**TX-116G118C-1** (SEQ ID NO:53 and 71; DNA and amino acid, respectively)

*Please replace the paragraph beginning at page 47, line 6 with the following amended*

*paragraph:*

Mutations identified above have been combined to create mutant xylanases with greater alkalophilicity and thermophilicity. The combination mutants xylanases based on quadruple mutations N11D/D116G/H144R/Q161R or N11D/Y118C/144R/Q161R, namely: TrX-H-11D-ML-75A105H-116G-125A129E-144R161R (TrX-H11D-ML-AHGAE-RR; Figure 9); and TrX-H-11D-ML-75A105H-118C-125A129E-144R161R (TrX-H11D-ML-AHCAE-RR; SEQ ID NO:55 not shown), exhibit a maximum enzymatic activity from about pH 5.5 to about pH 7, as compared to precursor xylanases. Furthermore the presence of the mutation D116G helps the retain substantially maximal activity at a lower pH range of 5.0, 5.5 and 6.0, thus avoiding the significant loss of activity at low pH as observed in precursor TrX-HML-75A105H-125A129E-144R161R (Figure 9). This result further ~~confirms~~ confirms the broadening of the optimal pH range.